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(21) International Application Number: PCT/EP00/04591 (22) International Filing Date: 4 May 2000 (04.05.00) (30) Priority Data: 60/132,705 5 May 1999 (05.05.99) US (71) Applicants (for all designated States except US): INSTITUT CURIE [FR/FR]; 26, rue d'Ulm, F-75248 Paris Cedex 05 (FR). CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.) [FR/FR]; 3, Rue Michel Ange, F-75794 Paris Cedex 16 (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): CAPPELLEN, David [FR/FR]; 8, avenue le Pont l'Evêque, F-14810 Merville-Franceville (FR). CHOPIN, Dominique [FR/FR]; 23, avenue de la Mame, F-94000 Creteil (FR). RAD-VANYI, François [FR/FR]; 36, rue des Potiers, F-92260 Fontenay-aux-Roses (FR). RICOL, David [FR/FR]; Bât. K, 40, rue Pascal, F-75013 Paris (FR). THIERY, Jean-Paul [FR/FR]; 16, rue Vandrezanne, F-75013 Paris (FR). (74) Agents: PEAUCELLE, Chantal et al.; Cabinet Armengaud Aîné, 3, avenue Bugeaud, F-75116 Paris (FR).		(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: MEANS FOR DETECTING AND TREATING PATHOLOGIES LINKED TO FGFR3		
(57) Abstract The invention relates to a method for detecting carcinomas in a biological sample, comprising identifying FGFR3 mutations.		

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Means for detecting and treating pathologies linked to FGFR3

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The invention relates to means, i.e. method and drugs, for detecting and treating, respectively, pathologies linked to FGFR3 and/or to the FGFR3 pathway.

Fibroblast growth factor receptor 3 (FGFR3) belongs to a family of
10 structurally related tyrosine kinase receptors (FGFRs 1-4) encoded by four different genes. These receptors are glycoproteins composed of two to three extracellular immunoglobulin (Ig)-like domains, a transmembrane domain and a split tyrosine-kinase domain. Alternative mRNA splicing results in many different receptors variants. Isoforms FGFR3-IIb and FGFR3-IIc result from a mutually exclusive splicing event in
15 which the second half of the juxtamembrane Ig-like domain is encoded either by the 151 nucleotides long exon 8 (IIb variant) or the 145 nucleotides long exon 9 (IIc variant).

Specific point mutations in the *FGFR3* gene which affect different domains of the protein are associated with autosomal dominant human skeletal disorders such as hypochondroplasia, achondroplasia, severe achondroplasia with developmental
20 delay and acanthosis nigricans and thanatophoric dysplasia. Several reports have demonstrated that these mutations lead to constitutive activation of the receptor. Taking into account this result, together with the skeletal overgrowth observed in mice homozygous for null alleles of *Fgfr3*, FGFR3 appears as a negative regulator of bone growth.

25 In contrast with this inhibitory role, an oncogenic role has been proposed for *FGFR3* in multiple myeloma (MM) development. In this malignant proliferation of plasma cells, a t(4;14)(p16.3;q32.3) chromosomal translocation with breakpoints located 50 to 100 Kb centromeric to *FGFR3* is present in 20-25% of the cases and is associated with overexpression of FGFR3.

30 In very rare cases (2 out of 12 MM cell lines and 1 out of 85 primary MM tumours), activating mutations of *FGFR3* previously identified in human skeletal disorders have been found, but always accompanied by the t(4;14)(p16.3;q32.3) translocation.

35 By investigating various cancers, the inventors have surprisingly found a role for FGFR3 in solid tumours, in particular in cancers originating from epithelial tissues, carcinomas.

The involvement of FGFR3 in such solid tumour development is linked to a constitutional activation : it may be activated by an autocrinal loop (ligand self-

production) and/or by activating mutations in *FGFR3*. Surprisingly, such mutations are found in primary tumours and are somatic mutations (genomic DNA mutations).

So far, the only *FGFR3* isoform which has been identified in epithelium is the *FGFR3*-IIIb isoform.

5 The invention thus relates to a method and kits for detecting such pathologies.

 According to another aspect, the invention also relates to drugs capable of treating such pathologies.

 According to still another aspect, it relates to transgenic animals enabling
10 the efficiency of such drugs to be tested as well as to cell lines transfected with the different forms of *FGFR3* (useful *in vitro* and *in vivo*).

 The method of the invention for detecting carcinomas in a biological sample comprises identifying *FGFR3* mutations.

 Standard methods can apply for such an identification such as
15 immunohistochemistry, or detection of the corresponding RNA, DNA, and encoded protein contained in said sample, particularly after extraction thereof. A common way for such a detection comprises amplifying by PCR, RT-PCR or RT-PCR SSCP (single strand conformation polymorphism) with *FGFR3* specific primers and revealing the amplification products according to the usual methods. A corresponding embodiment is
20 exemplified in the examples given hereinafter. Another common way comprises the use of antibodies and the detection of the antigen-antibody reaction with appropriate labelling.

 The activating function of a mutation can be determined by observation
of activating signals such as receptor phosphorylation, cell proliferation (e.g. thymidine
25 incorporation) or indirect effects such as calcium influx, phosphorylation of target sequences.

 More particularly, said identification comprises screening for single nucleotide mutation(s) in the genomic DNA and/or its products, i.e. RNA, protein, the term "product" also encompassing cDNA.

30 Particularly, said method comprises screening for mutations creating cysteine residues in the extracellular or transmembrane domains of the receptor.

 Alternatively, or in combination with the foregoing embodiment, it comprises screening for mutations resulting in at least one amino-acid substitution in the kinase domain of the receptor.

35 It particularly comprises screening of activating mutation(s) of *FGFR3*, notably such as above-described.

 More particularly, the method of the invention comprises screening for mutation(s) in exon 7, encoding the junction between immunoglobulin-like domains II

and III of FGFR3, in exon 10, encoding the transmembrane domain, in exon 15, encoding the tyrosine kinase domain I, and/or in the exon encoding the C-terminal part.

Advantageously, the method of the invention comprises screening for missense mutations such as implicated in thanatophoric dysplasia, NSC, achondroplasia, saddan, or hypochondroplasia.

Such FGFR3 mutations notably comprise R248C, S249C, G372C, S373C, Y375C, K652E, K652M, J809G, J809C, J809R, J809L, P250R, G377C, G382R, A393E, N542K (codons are numbered according to FGFR3-IIIb cDNA open reading frame).

The following FGFR3 mutations will be particularly identified : R248C, S249C, G372C, K652E and Y375C.

Said biological sample used in the method of the invention will advantageously comprise a tissue, bone marrow, or a fluid such as blood, urine, deriving from a warm-blooded animal, and more especially from a human.

Said method is particularly useful for detecting carcinomas, such as human bladder and cervix carcinomas. A major issue in superficial bladder cancer is to distinguish tumours which will progress from those which will not. Insights into the genetic and epigenetic alterations involved in bladder cancer is expected to provide useful information to facilitate this distinction. In that respect, the invention provides means to resolve the dilemma between a bladder-sparing strategy versus cystectomy and will contribute to a more individualised intravesical instillation and endoscopic monitoring policy.

Indeed, as shown by the results given in the examples, *FGFR3* appears to be a major oncogene in Ta, T1 bladder carcinomas. The *FGFR3* mutations appear to be frequently associated with tumours that do not progress. Multivariate analysis showed that *FGFR3* mutation status remained a statistically significant predictor of good outcome. *FGFR3* mutations thus provide clear-cut information, which may complement stage and grade. The use of these mutations alone and/or in combination with other predictors of tumour aggressiveness will then provide relevant prognostic information.

Said method, will also be used for detecting for example lung, breast, colon, skin cancers.

The method of detection according to the invention applies to the diagnostic of carcinomas, as well to the prognosis, or the follow-up of the efficiency of a therapy.

Said method will advantageously be performed by using kits comprising the appropriate reagents and a notice of use.

According to another aspect, the invention relates to drugs having an anti-proliferative effect on carcinoma cells. Such drugs comprise, as active principle(s)

agent(s) which act by inhibition of FGFR3 DNA synthesis or by inhibition of its expression products (RNA, proteins). Particularly, such drugs contain tyrosine kinase inhibitors specific for FGFR3.

Other appropriate inhibitors comprise antibodies directed against FGFR3, and particularly against at least one extracellular Ig-like domain thereof. Advantageously said antibodies are specific for FGFR3-IIIb. Preferred antibodies are monoclonal ones, and particularly antibodies modified so that they do not induce immunogenic reactions in a human body (e.g. humanized antibodies).

Other appropriate inhibitors comprise antisens oligonucleotides directed against a wild or mutated *FGFR3* isoform.

The administration and the posology of said inhibitors will be determined by the one skilled in the art depending on the carcinoma to be treated, the weight and age of the patient. For example, antibodies will be administered by the injectable route.

The invention thus gives means of great interest for detecting and treating carcinomas, taking into account the fact that cancers originating from epithelial tissues (carcinomas) represent approximately 90 % of malignant neoplasms.

The invention also relates to cell lines capable of expressing FGFR3 mutated forms. Particularly, the invention relates to FGFR3 S249C mutated forms. T24 cell lines constitutively expressing FGFR3 S249C mutated forms and HeLa cell lines expressing FGFR3 S249C mutated forms in an inducible manner have thus been obtained (for example see ref.(6)).

By injecting such cell lines to nude mice, an increased tumorigenicity was observed.

According to the invention, such cell lines are useful *in vitro* (follow up of the receptor phosphorylation) or *in vivo* (examination of the tumorigenicity of nude mice) to study the inhibitor effect against FGFR3.

Cell lines transfected with FGFR2, FGFR1 or FGFR4 are particularly useful for studying the specificity of inhibitors to be tested.

According to still another object, the invention relates to constructions capable of expressing by transgenesis a FGFR3 mutated form in epitheliums and the transgenic animals thus obtained which are characterized by the fact that they comprise such constructions.

Examples of constructions intended for injection in animal germinal cells comprise a keratin promoter, particularly keratin 14 promoter and cDNA of mutated FGFR3.

Other advantages and characteristics of the invention will be given in the following examples wherein it will be referred to

- figures 1A - 1B which give FGFR3-IIIb gene activating mutations in primary tumours,

- figures 2A - 2E which refer to FGFR3-IIIb wild (2A) and mutated pro-oncogenic (2B-2T) sequences. It will be noted that the sequences of figures 2B to 2T, as such, enter into the scope of the invention. There may be silent polymorphisms all along the sequence, so there may be in fact several possible sequences for each mutant, and

- figures 3a and 3b which respectively represent a) Kaplan-Meier progression-free survival curves according to *FGFR3* mutations (dotted line: mutated *FGFR3*, solid line: non-mutated *FGFR3*; log rank test $p=0.014$) ; b) Kaplan-Meier disease-specific survival curves according to *FGFR3* mutations (dotted line: mutated *FGFR3*, solid line: non-mutated *FGFR3*; log rank test $p=0.007$)

Example 1 : *FGFR3* gene mutations in bladder and cervix carcinomas

FGFR3-IIIb and *FGFR3-IIIc* transcript levels were examined by reverse transcription-polymerase chain reaction (RT-PCR) in 76 primary bladder carcinomas and 29 primary invasive cervical carcinomas.

FGFR3-IIIb, the sole isoform to be significantly expressed, was detected in 72 out of 76 (94%) bladder carcinomas and 27 out of 29 (93%) cervical carcinomas.

A PCR-SSCP analysis was then conducted on both reverse transcribed RNA and genomic DNA to screen for *FGFR3* coding sequence variants in 26 bladder and 12 cervix cancers expressing the gene. The results are illustrated in figures 1a and 1b which gives the identification of *FGFR3* gene mutations in human carcinomas :

- a: gives the identification of somatic mutations by direct sequencing of PCR products. Normal constitutional DNA ; Tumour, tumour DNA.

- b: gives *FGFR3* mutations associated with skeletal disorders and cancers.

The schematic structure of *FGFR3* is depicted (Ig I-III, immunoglobulin like domains ; TM, transmembrane domain ; TK-1 and -2, tyrosine kinase domains) and the locations of the known human missense mutations associated with thanatophoric dysplasia (TD) and severe achondroplasia (SADDAN), bladder and cervix carcinomas (carc.) and multiple myeloma (MM) are indicated. Usual amino acid abbreviations are used to point out the mutation found in each pathological situation. The mutations at codon 807 incriminated in TD replaces a Stop codon (J) by an amino acid (G, C, R or L) and the mRNA thus continues to be translated until another in-frame Stop codon is reached 423 nucleotides downstream thus leading to a 141 amino acid longer protein.

Abnormally migrating bands were observed for certain samples (Fig. 1a) and direct sequencing of PCR products revealed single nucleotide substitutions in 9 out of 26 bladder carcinomas (35 %) and 3 out of 12 (25 %) cervix carcinomas (Fig. 1b and table 1).

Table 1

Summary of FGFR3 gene mutations in primary bladder and cervix cancers					
Sample	Histopathol.	Codon	Nt Position	Mutation	Predicted effect
1447, bladder	carc., Ta G2	249	746	TCC to TGC	Ser to Cys
342, bladder	carc., T1a G1	249	746	TCC to TGC	Ser to Cys
813, bladder	carc., T1a G1	372	1114	GGC to TGC	Gly to Cys
1393.1, bladder	carc., T1a G3	249	746	TCC to TGC	Ser to Cys
506, bladder	carc., T1b G2	372	1114	GGC to TGC	Gly to Cys
1084, bladder	carc., T1b G3	652	1954	AAG to GAG	Lys to Glu
745.1, bladder	carc., T2 G3	248	742	CGC to TGC	Arg to Cys
1077, bladder	carc., T3 G2	249	746	TCC to TGC	Ser to Cys
1210, bladder	carc., T3 G2	249	746	TCC to TGC	Ser to Cys
4.13, cervix	carc., stage II	249	746	TCC to TGC	Ser to Cys
4.139, cervix	carc., stage II	249	746	TCC to TGC	Ser to Cys
6.96.1, cervix	carc., stage II	249	746	TCC to TGC	Ser to Cys

Histopathol., histopathological classification of the tumours (carc., carcinoma : TNM and HUGO classifications are used respectively for bladder and cervix cancers) ; codon and mutated nucleotide (Nt position) are numbered according to FGFR3-IIIb cDNA open reading frame.

Mutations were found in the following exons

- exon 7, encoding the junction between immunoglobulin-like domains II and III of FGFR3 (one C-to-T transition at codon 248 in patient 745.1 and a C-to-G substitution at codon 249 in patient 1447) ;

- exon 10, encoding the transmembrane domain (a G-to-T-transversion at codon 372 in patient 813)

- exon 15, encoding the tyrosine kinase domain II (a A-to-G transition at codon 652 in patient 1084).

Analysis of matched constitutional DNA from the patients for which such material was available (n=8) demonstrated the somatic nature of these *FGFR3* mutations (Figure 1).

Strikingly, each of the FGFR3 missense mutations identified herein, i.e. R248C, S249C, G372C and K652E, are implicated in thanatophoric dysplasia (TD).

Given the presence of two additional amino-acids in the IIb isoform expressed in epithelial cancers as compared to the IIc isoform expressed in bone, the G372C and K652E mutations are indeed equivalent to the G370C and K650E mutations responsible for TD.

5 The S249C mutation was the most commonly observed, affecting 5 out of 9 (55 %) bladder cancers and all of the cervical cancers (3 out of 3, 100 %) in which *FGFR3* gene alterations have been identified so far.

 The R248C, S249C and G372/370C mutations create cysteine residues in the extracellular or transmembrane domains of the receptor and the K652/650E mutations results in amino-acid substitution in the kinase domain of the receptor.

Example 2 : Inhibitors

 A way to test the different *FGFR3* inhibitors comprises transfecting cell lines so that they express the mutated forms of *FGFR3*, or wild type *FGFR3* or just the neomycin or hygromycin resistant gene under the control of a strong promoter, such as CMV, RSV, SV40 promoters. The tumorigenic properties of these cell lines can then be compared *in vitro* or *in vivo* in nude mice. The different inhibitors will be tested *in vitro* or *in vivo* using these different cell lines. Phosphorylation, proliferation or indirect effects of *FGFR3* such as calcium influx will be measured. Transgenic mice expressing in various epithelia the mutated *FGFR3* can thus be derived thereof. Those mice developing tumours are useful tools for testing the efficiency of candidate inhibiting drugs. Such transgenic animals fall also into the scope of the present invention.

Example 3 : *FGFR3* mutations in Ta, T1 tumours in bladder cancer.

 Bladder cancer is a disease with a spectrum of forms and is highly unpredictable. At the time of initial diagnosis, approximately 80% of patients present with a superficial tumour. Superficial bladder cancers include carcinoma *in situ* (Tis), Ta and T1 lesions (TNM classification). Ta/T1 lesions are mostly papillary urothelial carcinomas: Ta lesions do not invade the basement membrane, whereas T1 lesions invade the lamina propria, but do not invade the detrusor muscle of the bladder wall. Carcinoma *in situ* are flat, cytologically high-grade carcinomas, confined to the urothelium. Primary isolated carcinoma *in situ* is a very rare entity and is more commonly associated with Ta/T1 lesions. Despite transurethral resection alone or combined with adjuvant intravesical therapies, more than one half of patients with Ta/T1 tumours suffer recurrences. In most cases, recurrences are also superficial, but about 5% of Ta and 30-50% of T1 tumours progress in an unpredictable manner to muscle invasion with a high risk of development of metastases and death from bladder cancer.

 The management of superficial bladder cancer is based on clinicopathological parameters. Three groups of tumours can be defined. of low,

intermediate and high risk, according to their potential for recurrence and progression. This classification is used to recommend adjuvant intravesical therapies and bladder monitoring, but it is not a sufficiently sensitive discriminant for use in determining the appropriate treatment and mode of surveillance for a given patient. Although Bacille Calmette-Guérin (BCG) therapy appeared to be the most effective regimen for the high-risk group, long-term results indicate that progression occurs in 40% by 10 years and in more than 50% by 15 years. For some researchers, these findings justified the use of up-front radical cystectomy in high-risk superficial urothelial carcinomas, despite the risk of overtreating a significant number of patients. Follow-up of Ta and T1 superficial bladder cancers constitutes most of the workload of urologists involved in the management of bladder cancer. The current strategy is based on frequent cystoscopic evaluations using a schedule that is largely empirical, without considering the individual characteristics of the tumour.

The limitations of the current management of bladder cancer demonstrate the need for prognostic markers, making possible the use of selective aggressive treatments for patients at high risk of progression while sparing low-risk patients from unnecessary procedures. A number of chromosomal loci and specific genes have been implicated in bladder tumorigenesis. Losses of all or part of chromosome 9 in many TaG1 tumours suggests that the inactivation of a gene or genes on chromosome 9 may be an early event in urothelial transformation. The prognostic significance of losses on chromosome 9 is unclear. Alterations of the *P53* and *RB* genes controlling the G1 cell cycle checkpoint have been clearly delineated and are associated with the aggressiveness of superficial and invasive bladder cancers. Despite these recent insights into the molecular mechanisms of bladder carcinoma progression, these markers have not yet had any impact on clinical practice.

The following assays have been performed to assess the reliability, as markers, of the FGFR3 mutations.

Material and method

30 Patients and tissue samples

Seventy four specimens of superficial Ta, T1 bladder carcinomas were obtained from 74 patients by transurethral resection performed at the Henri Mondor hospital, Créteil, France, from January 1988 to December 1998. Tumours were staged according to the TNM classification (1) and graded according to criteria recommended by the World Health Organisation (2). This series consisted of 25 pTa and 49 pT1 tumours, with 28 grade G1, 33 grade G2 and 13 grade G3 tumours. The 64 men and 10 women had a mean age of 64 years (range: 29 to 94 years). None of the patients had any detectable distant metastases at the time of transurethral resection. Patients were treated

by transurethral resection (TUR) alone (n=25), TUR followed by mitomycin C instillation (n=10) or TUR and BCG (n=39) according to the French Committee for Urologic Oncology (CCAFU) recommendations. There was no change in the policy for treating superficial bladder cancer during the study period. Progression was defined as the occurrence of a pT2 or higher stage or appearance of lymph node invasion or metastasis or death from cancer. Disease-specific survival curves were plotted using death from urothelial cancer as the endpoint. Follow-up was based on systematic cystoscopy and cytology, and imaging studies only when indicated. All outpatient visits and hospital admissions were recorded in a database from which the study data were calculated.

Tumour DNA was extracted from formalin-fixed and paraffin-embedded tissue or samples freshly frozen in liquid nitrogen (4). Normal DNA samples from peripheral blood were available for 27 patients.

15 *FGFR3* mutation analysis

Mutations in the *FGFR3* gene were detected by SSCP analysis. Exons 7, 10, 15 and 20 of the *FGFR3* gene were analysed because these exons harbour all the mutations previously identified in bladder carcinomas and thanatophoric dysplasia. All mutations detected by SSCP analysis were confirmed by direct bidirectional sequencing of tumour genomic DNA. Matched normal DNA, if available, was sequenced on both strands to demonstrate the somatic nature of these mutations.

Statistical methods

Associations between *FGFR3* mutation status and other data (sex, age, stage and grade) were tested using χ^2 and Student's t tests. Progression-free and disease-specific survival curves were plotted using Kaplan-Meier estimates. Survival distributions were compared using the log-rank test. Cox's proportional hazards regression model was used to test the effect of mutations, while simultaneously accounting for baseline patient and tumour characteristics. The influence of the covariates on the *FGFR3* mutation effect was assessed in multivariate analysis involving a forward stepwise procedure and a backward stepwise procedure, using the MPRL (maximum partial likelihood ratio) method. The limit to enter a term was 0.15 and the limit to remove a term was 0.10. Statistical analyses were performed using BMDP® and S-Plus® software.

Results

FGFR3 missense mutations were observed in 41 of the 74 (55%) Ta, T1 bladder tumours. The *FGFR3* mutations found are described in Table 2 below :

Table 2

Number of tumours (%)	Codon*	nt position*	Mutation	Predicted effect
5 (12%)	248	742	CGC -> TGC	Arg -> Cys
28 (68.5%)	249	746	TCC -> TGC	Ser -> Cys
5 (12%)	372	1,114	GGC -> TGC	Gly -> Cys
2 (5%)	375	1,124	TAT -> TGT	Tyr -> Cys
1 (2.5%)	652	1,954	AAG -> GAG	Lys -> Glu

* codon and mutated nucleotide (nt position) are numbered according to FGFR3-IIIb cDNA open reading frame. FGFR3-IIIb is the isoform expressed in epithelial cells.

5

S249C was the commonest mutation and was found in 16 of the 21 (76%) mutated Ta tumours and 12 of the 20 (60%) mutated T1 tumours. Matched constitutional DNA, available in 15 of the cases of tumour with mutations, contained wild-type sequences, demonstrating the somatic nature of these mutations.

10

The correlation between sex, age, stage, grade and *FGFR3* mutation status is given Table 3 :

Table 3

	<i>FGFR3</i> wild type	<i>FGFR3</i> mutant	p value (χ^2 or Student's t test)
Sex			
Male	29	35	
Female	4	6	0.9779
Age (years)			
mean	64.30	63.22	
range	[29.15-86.10]	[34.3-94.4]	0.7393
Stage			
Ta	4	21	
T1	29	20	0.001
Grade			
G1	7	21	
G2	14	19	
G3	12	1	0.0003

Statistically significant correlations were observed between *FGFR3* mutations and low stage (p=0.001) and low grade (p=0.0003), but not between these mutations and age or sex (Table 2).

With a median follow-up of 4.3 years (range: 6 months to 11 years), 3 patients progressed and one died in the mutated tumour group (n=41 patients) whereas ten patients progressed and eight died in the non-mutated tumour group (n=33 patients).

The median follow-up was 5.6 years (range: 7 months to 11 years) in the non-mutated group and 4.1 years (range: 6 months to 9 years) in the mutated group.

To examine *FGFR3* mutations as a marker of patient outcome, we calculated Kaplan-Meier progression-free survival and disease-specific survival probability curves for the two groups of patients and examined the differences using the log rank test. Progression-free and disease-specific survival indicated that *FGFR3* mutations were associated with a lower risk of progression ($p=0.014$) and longer survival ($p=0.007$) (Figure 3). We tested several variables (age, sex, stage, grade) but only stage was significantly associated with progression and survival in univariate analysis. If only T1 patients were analysed, the correlation was still significant for disease-specific survival ($p=0.03$) and close to significance for progression-free survival ($p=0.052$).

Multivariate analysis was used to determine whether the correlation between *FGFR3* mutation status and progression-free survival or disease-specific survival was independent of other outcome predictors. For progression-free survival, the following covariates were introduced into the Cox model: mutation, stage, grade and sex. For disease-specific survival, mutation and grade were the only covariates introduced into the model, as no disease-related deaths were observed among female or Ta patients. If *FGFR3* status was entered into the model, neither stage nor grade provided any additional prognostic value for tumour progression. In the analysis of disease-specific survival, *FGFR3* mutation was also the only covariate to be entered into the model, as grade did not provide any additional prognostic information. Relative risks and their 95% confidence intervals (CI) are shown in Table 4.

Table 4

	Progression		Disease-specific Survival	
	Relative Risk	95% CI	Relative Risk	95% CI
<i>FGFR3</i>				
Wild-type	1		1	
Mutant	0.23	(0.06; 0.83)	0.10	(0.01; 0.80)
Other variables do not significantly contribute to the model				

Forward and backward procedures both yielded the same model.

As shown by the above results, the FGFR3 activating mutations were frequent in bladder carcinomas.

All the carcinomas having a mutated receptor expressed said receptor at levels similar or above those observed with normal tissues. Immunohistochemical methods will then advantageously be used for revealing the receptor.

FGFR3 mutation detection in bladder carcinomas appears to be a good pronostic, giving then to the clinicians valuable means for treating and observing carcinomas, which represent a medical problem due to the high frequency of recurrences.

By using SSCP or PCR coupled to an enzymatic restriction S249C mutation specific (which represent 75% of the mutations) on patients having bladder carcinomas with S249C mutation, the mutation could be detected in urine in 60% of the cases.

Example 4: Detection of FGFR3 mutations in patients' urines

Genomic DNA is extracted from patients' urines and amplified by PCR, in the presence of ³²P- labelled dCTP, using standard methods. The following primers were used for detecting S249C mutation :

5'-CAG CAC CGC CGT CTG GTT GG-3' and 5'-AGT GGC GGT GGT GGT GAG GGA G-3'.

30 cycles of PCR are performed.

The amplification products are digested by *Cac8I*. An additional site is created by *FGFR3* mutation and a corresponding band is observed on an electrophoretic gel.

Similarly the following primers and enzymes can be used to detect :

R248C mutation :

Primers : 5'-TGT GCG TCA CTG TAC ACC TTG CAG-3' and 5'-AGT GGC GGT GGT GGT GAG GGA G-3'

Enzyme : *Bsi* HKA I

K652E mutation :

Primers : 5'-TGG TGA CCG AGG ACA ACG TGA TG-3' and 5'-AGG GTG TGG GAA GGC GGT GTT G-3'

Enzyme : *Bsm* A I

G372C mutation :

Primers : 5'-CCT CAA CGC CCA TGT CTT TTC AGC-3' and 5'-CTT GAG CGG GAA GCG GGA GAT CTT G-3'

Enzyme : *Pst* I

Y375C mutation :

Primers : 5'-CCT CAA CGC CCA TGT CTT TTC AGC-3' and 5'-CTT GAG CGG
GAA GCG GGA GAT CTT G-3'

5 Enzyme : *Bsg* I

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CLAIMS

1/ A method for detecting carcinomas in a biological sample, comprising
5 identifying FGFR3 mutations.

2/ The method of claim 1, comprising screening for single nucleotide
mutation(s) in nucleic acids of the group comprising genomic DNA, RNA or cDNA.

10 3/ The method of claim 1, comprising screening for single mutation(s) in
proteins.

4/ The method of claim 1, comprising screening for mutations creating cysteine
residues in the extracellular or transmembrane domains of the receptor.

15 5/ The method of claim 1, comprising screening for mutations resulting in at
least one amino-acid substitution in the kinase domain of the receptor.

20 6/ The method of claim 5, comprising screening of activating mutation(s) of
FGFR3.

7/ The method of claim 6, comprising screening of activating mutation(s) of
FGFR3-IIIb.

25 8/ The method of claim 1, comprising screening for mutation(s) in the group
comprising exon 7, encoding the junction between immunoglobulin-like domains II and
III of FGFR3, exon 10, encoding the transmembrane domain, exon 15, encoding the
tyrosine kinase domain I, and the exon encoding the C-terminal part.

30 9/ The method of claim 1, comprising screening for missense mutations such as
implicated in thanatophoric dysplasia, NSC, achondroplasia, SADDAN, or
hypochondroplasia.

35 10/ The method of claim 9, wherein the mutations comprise R248C, S249C,
G372C, S373C, Y375C, K652E, K652M, J809G, J809C, J809R, J809L, P250R,
G377C, G382R, A393E, N542K.

11/ The method of claim 9, comprising screening R248C, S249C, G372C, K652E and Y375C mutations.

12/ The method of claim 1, wherein the biological sample is selected in the group comprising a tissue, bone marrow, or a body fluid.

13/ The method of claim 12, wherein said body fluid is selected in the group comprising blood, urine from a warm-blooded animal.

14/ The method of claim 13, wherein said body fluid is from a human.

15/ The method of claim 1 for detecting human bladder and cervix carcinomas.

16/ The method of claim 1, for detecting lung, breast, colon, skin cancers.

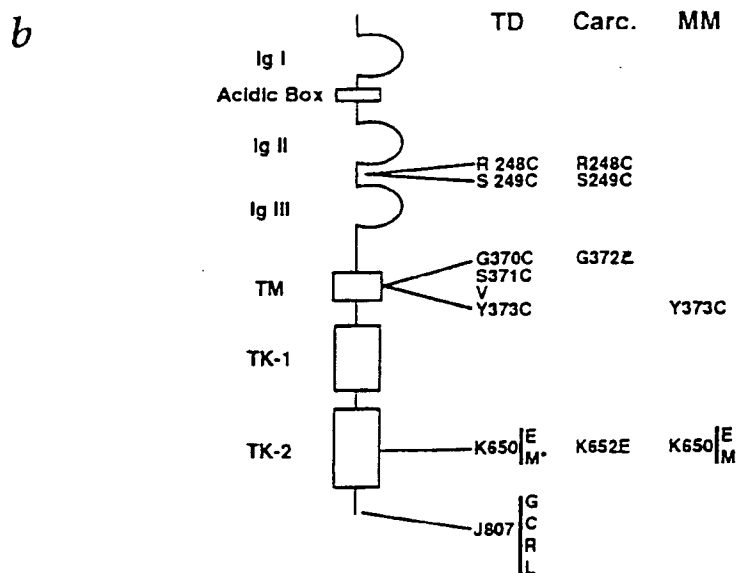
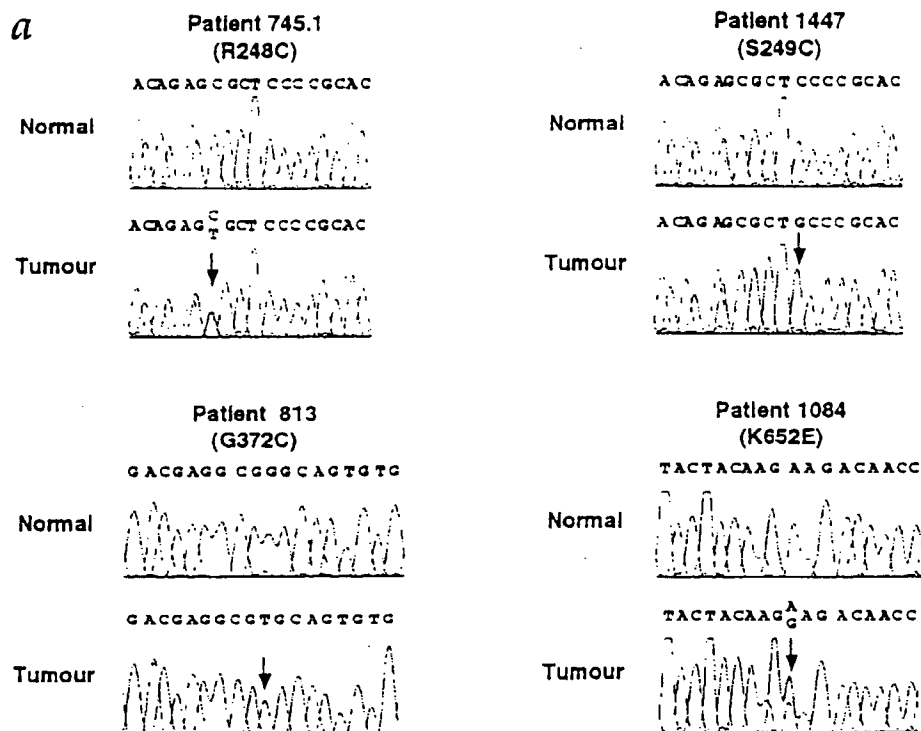
17/ The pharmaceutical preparations having an anti-proliferative effect on carcinoma cells comprising an effective amount of agent(s) which act by inhibition of FGFR3 DNA synthesis or by inhibition of its expression products.

18/ The pharmaceutical preparations of claim 17, comprising tyrosine kinase inhibitors specific for FGFR3.

19/ The pharmaceutical preparation of claim 18, comprising antibodies directed againstp FGFR3.

20/ The pharmaceutical preparations of claim 17, comprising antisens oligonucleotides directed against a wild type or mutated FGFR3 isoform.

FIGURE 1



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Figure 2A

Wild Type FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCTTGGGGAC
GGAGCAGCGCTCGTGGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGCGCGTGGCGGCCCAACACCGTCCGCTTCCGCTGCCAGCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCAGCACCAGTGGAGGATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCTCGGACCGGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCGCACCGGCCATCCTGCAGGCGGGGCTGCCGGCCAACCAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCGGACGGCACACCCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCAGGGCCCCGAGCAGCCGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCACCCTGCACAAGATCTCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCCTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCCT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGGC
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGGCCCCCGGGCCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCGGGCATGGAGTACTTGGCCTCCAGA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGCTCGCGGACGTGA

Figure 2B

Mutant R248C FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCGTGGGCGGAGCGGCAGAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCCGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCTA
CAGCTGCCGCGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCCCTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCAACACCGTCCGCTTCCGCTGCCAGCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGGCGAGCACCCGATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCGTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGTGTCCCCGACCGGCCATCCTGCAGGCGGGGCTGCCGGCCAACCAGACGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCTACGTTACCGTGTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTCGGAGCGGGACGGGGCGAGTACCTCTGTCGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCCTTTTGGCTGAGCGTTACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCCCCAAGAAAGGCTGGGCTCCCCACCGTGCACAAGATCTCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCGTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGCGGCCCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGATGGAGTACTTGGCCTCCGAGA
AGTGCATCCACAGGGACCTGGCTGCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACAGCCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGCCACGACCTGCTGCCCCGGCCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

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Figure 2C

Mutant S249C FGFR3-IIIb:

ATGGGCGCCCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGCGCCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCCGGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCGCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCCTA
CAGCTGCCGCGAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCGGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAAGCGCAGGGAGTTCCGCGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTGCCCGCACCGGCCCATCCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCTTACGTTACCGTGTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCCTTTTGGCTGAGCGTTACCGGGCCCCGAGCAGCCGAGGAGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCCCCAAGAAAGGCTGGGCTCCCCACCGTGCAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTCGGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGCCCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCCTACCAGGTGGCCCCGGGGCATGGAGTACTTGGCCTCCAGA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTACCCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGGCTCGCGGACGTGA

Figure 2D

Mutant G372C FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCTCGTGGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCGAGCGGTGCAGGTGCTGAATGGCTCCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCGCTGCCAGCCSCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGGCGGCGAGCACCAGATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTGGTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGAGCTGTGGAGCGCTCCCGCACCGGCCCATCTGCAGGCGGGGCTGCCGGCAACAGACGGCGGTGCT
GGGCAGCGAGTGGAGTTCCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCGCGGACGGCACACCTACGTTACCGTGTCAAGTCTTGGATCAGTGAGAGTGTGGAGGCGGAC
GTGGCCTCCGCTGGCCAATGTGTGGAGCGGGACGGGGCGAGTACCTCTGTGGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGTGCAGTG
TGATGCAAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTCATCTGCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCAACGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGTAACCTGCGGGAGTTTCTGCGGGCGCGGGCGCCCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCAGA
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTGCCACGACCTGCTGCCCGGGCCCCA
CCCAGCAGTGGGGGCTCGCGGACGTGA

Figure 2E

Mutant K652E FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAGTCCCGGGCCAGAGCCCGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGTGCCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCGAGCACCCGATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCACCGGCCATCCTGCAGGCGGGGCTGCCGGCCAACCAGACGGCGGTGCT
GGCAGCGACGTGGAGTTCACCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCGGACGGCACACCCTACGTTACCGTGTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTACGGGGCCCCGAGCAGCCGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCTGGGCTCCCCCACCCTGCACAAGATCTCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCGGCTGACCTGGGCAAGCCCCCT
GGGAGGGGCTGCTTCGGCCAGGTGGTGTGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCAAGCCTGTCAACCT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCGGGGATGGAGTACTTGGCCTCCCAGA
AGTGCATCCACAGGGACCTGGCTGCCCCTGATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGGAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTACCCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

Figure 2F

Mutant S373C FGFR3-IIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGCCGTGCGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCAGAGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAAGCGCAGGGAGTCCCGGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTCTGGGAGAACAAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCACCGGCCCATCCTGCAGGGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGGCCGGACGGCACACCTACGTTACCGTGTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTACGCGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGCGGGCTGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCTGGGCTCCCCACCGTGACACAAGATCTCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCAAGCCTGTCACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGGCCCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACAGGTGGCCCGGGGCGATGGAGTACTTGGCCTCCAGAG
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCACTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

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Figure 2G

Mutant Y375C FGFR3-IIb:

ATGGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGGCGAGCGGCAGAACTCCCGGGCCAGAGCCCGGCCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCGGGGTGGTCCCATGGGGCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGGCCCTCGGAGCGTGTCTGTTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCCGGGCGAGCACCGCATTTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCCCTCGGACCGCGGCAACTACACCTGCGTCTGTTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCGCACCGGCCCATCTGCAGGCGGGGCTGCCGGCCAACGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCACTCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACCCCTACGTTACCGTGTCAAGTCTCGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTCATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTGTGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCACCGTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCCTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCGGGCATGGAGTACTTGGCCTCCGAGA
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCCTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCACTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGCTCGCGGACGTGA

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Figure 2H

Mutant K652M FGFR3-IIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGTGCAGGTGCTGAATGCCTCCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGTACAGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCGGGCCGCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGGGCAGCACCGCATTTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAAGTTTGGCAGCATCCGGCAGACC
TACACGCTGGACGTGCTGGAGCGTCCCCGACCGGCCCATCCTGCAGGCGGGGTGCGGGCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCTCCGCTCGGCAATGTGTGGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTCATCCTGGTGGTGGCGGTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGTGACCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGGGCGGGCCCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACAGGTGGCCGGGGCATGGAGTACTTGGCCTCCCAGA
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGATGACAACCAACGGCCGGCTGCCCCGTGAAGTGGATGGCGCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCACTCCAGCTCCTCAGGGGACGACTCCGTGTTTCCCACGACCTGCTGCCCCGGGCCCCA
CCCAGCAGTGGGGGCTCGCGGACGTGA

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Figure 2I

Mutant X809C FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGCGCGTGGCCATCSTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCGCCGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCCTA
CAGCTGCCCGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGACCGGGCCATCCTGCAGGCGGGGCTGCCGGCCAAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCGGACGGCACACCTACGTTACCGTGCTCAAGTCTTGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGECATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGGGCGGGCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCAGA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGCGCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCCAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGGCTCGCGGACGTGC

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Figure 2J Mutant 1

Mutant X809G FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCSCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCGGGCCCGAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCAGAGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGACTCCGGGGCCTA
CAGCTGCCCGCAGCGGCTCAGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCGAGCACCGCATGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGACCGGCCCATCCTGCAGGCGGGGCTGCCGGCCAAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCCTACGTTACCGTGCTCAAGTCCCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGCC
CGAGAAGGCCTTTTGGCTGAGCGTTCAGGGCCCCGAGCAGCCGAGGAGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCAGAG
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCGAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGGCTCGCGGACGGGA

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Figure 2K Mutant 2

Mutant: X809G FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTGGGGCGAGCGGCAGAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCGCCGGGGTGGTCCCATGGGGCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGTGGGGCCCCAGCGGGTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCAGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACCCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCCAACTACACCTGCGTCTGTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGACCGGCCCATCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCCTACGTTACCGTGCTCAAGTCCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGGAGCGGGACGGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCCCCAAGAAAGGCTGGGCTCCCCACCGTGACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGGCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCAGA
AGTGCAATCCACAGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCTGAGGC
CTTGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGCTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTGCCACGACCTGCTGCCCCGGGCCCA
CCCAGCAGTGGGGGCTCGCGGACGAGA

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Figure 2L Mutant 3

Mutant X809G FGFR3-IIIB:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGCGCCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCTGCTGGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCACGCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAAGCGCAGGGAGTTCCGCGCGCAGCACCGCATTTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCCCTCGGACCGCGGCAACTACACCTGCGTCTGTGGAGAACAAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCGCACCAGGCCCATCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGGCCCGACGGCACACCCCTACGTTACCGTGTCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCTCCGCTGGCCAAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTACGCGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGTGGGCTTCTTCTCTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCTGGGCTCCCCACCCTGCACAAGATCTCCGCTTCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTCAATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCTGCACGAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGCGGCCCCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCAGA
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTCCGGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCCGGCCCA
CCAGCAGTGGGGGCTCGCGGACGCGA

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Figure 2M

Mutant X809L FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCGTGGGGCGAGCGGCAGAAGTCCC GGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGTTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGCGAGCACCAGTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCACCGGCCCATCTGCAGGCGGGGCTGCCGGCCAAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCACCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGTGGGCGCGGACGGCACACCTACGTTACCGTGTCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAAATGTGTGCGAGCGGGACGGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGCGGTGGC
CGAGAAGGCCCTTTGGCTGAGCGTTACGGGCCCCGAGCAGCGGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCAGCGTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGGCCCAAGCCTGTCAACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTCCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGGCCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACCCCCAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGCCCCA
CCAGCAGTGGGGGCTCGCGGACGTTA

Figure 2N Mutant 1

Mutant N542K FGFR3-IIIB:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCGCGCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCCACGAGGACTCCGGGGCCTA
CAGCTGCCGCGAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCAACCGGCCATCCTGCAGGCGGGGCTGCCGGCCCAACCAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCACCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCCCTACGTTACCGTGCTCAAGTCTTGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTCGGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGCGGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCTCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGCACAAGATCTCCCGCTTCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGAGGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTCGGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAAACTGCTGGGCGCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGCCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTGGGGCTG
GCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGG
GCTCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTGCCACGACCTGCTGCCCCGGCCCCA
CCCAGCAGTGGGGCTCGCGGACGTGA

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Figure 20 Mutant 2

Mutant N542K EGFR3-IIIb:

ATGGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCCTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTGGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAATTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGGCCCTCGGAGCGTGTCTGGTGGGGCCCGAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACCACCGTCCGCTTCGCGTGGCCAGCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCCGCGGCAGCACCCGATTTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCTCGGACCGCGGCAACTACACCTGCGTGGTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCGGCACCGGCCCATCTGCAGCGGGGGCTGCCGGCCAAACCAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCCCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCATGTGTGGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCCTTTGGCTGAGCGTTACCGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCTCAGCTACGGGGTGGGCTTCTTCTGTTCATCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCACCCTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCCTGGGCAAGCCCTT
GGGGAGGSGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAAGCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGGC
GCCAAGGTTAACCTGCGGGAGTTTCTGCGGGCGCGGGCCCCCGGGCCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCGA
AGTGCATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACACGCTGATGAAGATCGCAGACTTCGGGCTG
GCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAA
TGACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGGCGCCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCAGCTCCAGCTCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCCGGGCCCA
CCCAGCAGTGGGGCTCGCGGACGTGA

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Figure 2P Mutant 1

Mutant G382R FGFR3-IIIb:

ATGGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCGTGGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGSCTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCAACACCGTCCGCTTCCGCTGCCAGCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGAGTTCCGCGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCACCGGCCCATCCTGCAGGCGGGGCTGCCGGCCAAACCAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCGGACGGCACACCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGGCGAGTACCTCTGTGAGCCACCAATTTATAGCGGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTCACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACAGGCTGGGCTTCTTCTGTTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCACCCTGCACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCTGGGCAAGCCCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCCGCAAGCCTGTACCCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGGCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTTACCAGGTGGCCCCGGGGCATGGAGTACTTGGCTCCCAGA
AGTGCATCCACAGGGACCTGGCTGCCCCGAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGGAGCTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCTGAGGC
CTTGTGTTGACCGAGTCTACACTACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCCGCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCTTTTCAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCGGGCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

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Figure 2Q Mutant 2

Mutant G382R FGFR3-IIIb:

ATGGGCGCCCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACAGGAGTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACAGGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGCGGAGCACCAGTTCAGTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGTGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGACCGGCCCATCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCACATCCAGTGGCTCAAGCAGTGGAGGTGA
ACGGCAGCAAGGTGGGCGCGGACGGCACACCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCCTTTTGGCTGAGCGTTACCGGGCCCCGAGCAGCCGAGGAGGAGTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACCGGGTGGGCTTCTTCTGTTTCATCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCCCCAAGAAAGCGCTGGGCTCCCCACCGTGCAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACCGCTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCCAGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCCTT
GGGGAGGGTGTCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGGC
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGGGCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCGGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCAGA
AGTGTCATCCACAGGGACCTGGCTGCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCCGGCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

Figure 2R

Mutant G377C FGFR3-IIib:

ATGGGCGCCCTGCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGGCCCTTACTGGACACGGCCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGGCGAGCACCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGACCGGCCCATCCTGCAGGCGGGGGTCCCGGCCAACCAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCCGACGGCACACCCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGGCGAGTACCTCTGTGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTACGGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCATGCATCCTCAGCTACGGGGTGGGCTTCTCTGTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCCACCCTGCACAAGATCTCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGGGCCCGGGCTGGACTACTCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCCAGA
AGTGACATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCCGGCTG
GCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTGTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGCGCCTTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCACGACCTGCTGCCCCCGGCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

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Figure 25

Mutant A393E FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCGTCTGTGGGCGAGCGGCAGAAAGTCCCGGGCCAGAGCCCGGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCGGGGGTGGTCCCATGGGGCCCACTGTCTGGGTCAAGGATGGCACAGGG
CTGGTGGCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGTGCAGGTGCTGAATGCCTCCACGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCTTACTGGACACGGCCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCGCGGGCAGCACCAGCATGAGGATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGGCCTCGGACCGCGGCAACTACACCTGCTGCTGGAGAACAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCCGCACCGGCCATCCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGGCCGGACGGCACACCCTACGTTACCGTGCTCAAGTCTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCCTGGCCAATGTGTGCGAGCGGGACGGGGGCGAGTACCTCTGTCGAGCCACCAATTTTCATAGGCGTGGC
CGAGAAGGCCTTTTGGCTGAGCGTTACGGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTCATCCTGGTGGTGGAGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCTGGGCTCCCCACCGTGACACAAGATCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCTT
GGGGAGGGCTGCTTCGGCCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTCCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAAACATCATCAACCTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGGCCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACAGGTGGCCCGGGCATGGAGTACTTGGCCTCCAGA
AGTGATCCACAGGGACCTGGCTGCCCCGAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCGGACGTGACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTCACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAAC
TGACACACGACCTGTACATGATCATGCGGGAGTGCTGGCATGCCGCGCCCTCCAGAGGCCACCTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCCTTTCGAGCAGTACTCC
CGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGGACGACTCCGTGTTTGGCCAGACCTGCTGCCCCGGGCCCA
CCAGCAGTGGGGCTCGCGGACGTGA

Figure 2T

Mutant P250R FGFR3-IIIb:

ATGGGCGCCCTGCCTGCGCCCTCGCGCTCTGCGTGGCCGTGGCCATCGTGGCCGCGCCTCCTCGGAGTCCTTGGGGAC
GGAGCAGCGCTCGTGGGCGAGCGGCAGAAGTCCCGGGCCAGAGCCCGCCAGCAGGAGCAGTTGGTCTTCGGCAGCG
GGGATGCTGTGGAGCTGAGCTGTCCCCCGCCGGGGTGGTCCCATGGGGCCACTGTCTGGGTCAAGGATGGCAGAGG
CTGGTGCCCTCGGAGCGTGTCTGGTGGGGCCCCAGCGGTGCAGGTGCTGAATGCCTCCACAGAGGACTCCGGGGCCTA
CAGCTGCCGGCAGCGGCTCACGCAGCGCTACTGTGCCACTTCAGTGTGCGGGTGACAGACGCTCCATCCTCGGGAGATG
ACGAAGACGGGGAGGACGAGGCTGAGGACACAGGTGTGGACACAGGGGCCCCCTTACTGGACACGGGCGAGCGGATGGAC
AAGAAGCTGCTGGCCGTGCCGGCCCAACACCGTCCGCTTCCGCTGCCAGCCGCTGGCAACCCCACTCCCTCCATCTC
CTGGCTGAAGAACGGCAGGGAGTTCCGCGGCGAGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCAGTGGAGCCTGG
TCATGGAAAGCGTGGTGCCTCGGACCGCGGCAACTACACCTGCGTCTGGAGAACAAAGTTTGGCAGCATCCGGCAGACG
TACACGCTGGACGTGCTGGAGCGCTCCCGGCACCGGCCCATCCTGCAGGCGGGGCTGCCGGCCAACAGACGGCGGTGCT
GGGCAGCGACGTGGAGTTCCTACTGCAAGGTGTACAGTGACGCACAGCCCCACATCCAGTGGCTCAAGCACGTGGAGGTGA
ACGGCAGCAAGGTGGGCCCGGACGGGCACACCTACGTTACCGTGCTCAAGTCTTGGATCAGTGAGAGTGTGGAGGCCGAC
GTGCGCCTCCGCTGGCCAATGTGTGCGAGCGGGACGGGGCGAGTACCTCTGTGAGCCACCAATTTTATAGGCGTGGC
CGAGAAGGCCCTTTTGGCTGAGCGTTACGGGCCCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTG
TGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCTGTTTATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCTG
CGCAGCCCCCAAGAAAGGCCCTGGGCTCCCCCACCCTGCACAAGATCTCCGCTTCCGCTCAAGCGACAGGTGTCCCT
GGAGTCCAACCGCTCCATGAGCTCCAACACACCACTGGTGGCATCGCAAGGCTGTCTCAGGGGAGGGCCCCACGCTGG
CCAATGTCTCCGAGCTCGAGCTGCCTGCCGACCCCAATGGGAGCTGTCTCGGGCCCGGCTGACCTGGGCAAGCCCCCTT
GGGGAGGGCTGCTTCCGGCAGGTGGTTCATGGCGGAGGCCATCGGCATTGACAAGGACCGGGCCCAAGCCTGTACCGT
AGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGACCTGTGCGACCTGGTGTCTGAGATGGAGATGATGAAGATGA
TCGGGAAACACAAAACATCATCAACTGCTGGGCGCCTGCACGCAGGGCGGGCCCCCTGTACGTGCTGGTGGAGTACGCG
GCCAAGGGTAACCTGCGGGAGTTTCTGCGGGCGCGGCGCCCCCGGGCTGGACTACTCCTTCGACACCTGCAAGCCGCC
CGAGGAGCAGCTCACCTTCAAGGACCTGGTGTCTGTGCTACCAGGTGGCCCGGGGCATGGAGTACTTGGCCTCCGAGA
AGTGATCCACAGGGACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACAACGTGATGAAGATCGCAGACTTCGGGCTG
GCCCCGGGACGTGCACAACCTCGACTACTACAAGAAGACAACCAACGGCCGGCTGCCGTGAAGTGGATGGCGCCTGAGGC
CTTGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGGTCTTTGGGGTCTGCTCTGGGAGATCTTACGCTGGGGG
GCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCGCCAAC
TGCACACACGACCTGTACATGATCATGCGGGAGTGTGGCATGCCGCGCCCTCCAGAGGCCCACTTCAAGCAGCTGGT
GGAGGACCTGGACCGTGTCTTACCGTGACGTCCACCGACGAGTACCTGGACCTGTGCGGCGCTTTCGAGCAGTACTCCC
CGGGTGGCCAGGACACCCCAAGCTCCAGCTCCTCAGGGACGACTCCGTGTTGCCACGACCTGTGCCCCGGCCCCA
CCAGCAGTGGGGGCTCGCGGACGTGA

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FIGURE 3

